```
### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 01.07.09D

Last logoff:  11aug01 14:05:03
Logon file001 12aug01 10:28:28
           *** ANNOUNCEMENT ***
                    ***
--Important Notice to Freelance Authors--
See HELP FREELANCE for more information
                    ***
NEW FILE RELEASED
***EIU Business Magazines (File 622)
***IBISWorld Market Research (File 753)
***Investext PDF Index (File 745)
***Daily and Sunday Telegraph (London) Papers (File 756)
***The Mirror Group Publications (United Kingdom) (File 757)

UPDATING RESUMED
***Delphes European Business (File 481)
***Books In Print (File 470)
                             ***
RELOADED
***Kompass Middle East/Africa/Mediterranean (File 585)
***Kompass Asia/Pacific (File 592)
***Kompass Central/Eastern Europe (File 593)
***Kompass Canada (File 594)
***CANCERLIT (File 159)
***Information Science Abstracts (File 202)

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   wire.  First Release provides full Dialog searchability
   and full-text features.  To search First Release files in
   OneSearch simply BEGIN FIRST for coverage from Dialog's
   broad spectrum of news wires.

     >>> Enter BEGIN HOMEBASE for Dialog Announcements <<<
     >>>    of new databases, price changes, etc.      <<<
                    ****
KWIC is set to 50.
HILIGHT set on as '*'
 *** F222 is temporarily unavailable ***

File   1:ERIC  1966-2001/Aug 06
       (c) format only 2001 The Dialog Corporation

      Set  Items  Description
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?b 434, 5, 155
       12aug01 10:28:32 User259980 Session D144.1
            $0.23    0.065 DialUnits File1
     $0.23  Estimated cost File1
     $0.23  Estimated cost this search
     $0.23  Estimated total session cost   0.065 DialUnits
```

```
SYSTEM:OS  - DIALOG OneSearch
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
        (c) 1998 Inst for Sci Info
  File   5:Biosis Previews(R)  1969-2001/Aug W1
        (c) 2001 BIOSIS
  File 155:MEDLINE(R)  1966-2001/Sep W1

      Set  Items  Description
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?e au=ueki

Ref   Items  Index-term
E1        1  AU=UEKERT S
E2        1  AU=UEKESA T
E3        9 *AU=UEKI
E4      320  AU=UEKI A
E5        2  AU=UEKI AKIHARU
E6       12  AU=UEKI AKINORI
E7        1  AU=UEKI AKIO
E8        1  AU=UEKI AKIR
E9       28  AU=UEKI AKIRA
E10       6  AU=UEKI ATSUKO
E11       1  AU=UEKI ATSUSHI
E12       1  AU=UEKI ATUKO

          Enter P or PAGE for more
?p

Ref   Items  Index-term
E13      22  AU=UEKI AYAKO
E14       2  AU=UEKI BH
E15       2  AU=UEKI E
E16       1  AU=UEKI F
E17     580  AU=UEKI H
E18       1  AU=UEKI HIDEAKI
E19       2  AU=UEKI HIDENORI
E20      26  AU=UEKI HIROAKI
E21       4  AU=UEKI HIROFUMI
E22       3  AU=UEKI HIRONORI
E23      18  AU=UEKI HIROSHI
E24      70  AU=UEKI I

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Ref   Items  Index-term
E25      38  AU=UEKI I F
E26      64  AU=UEKI IF
E27       2  AU=UEKI IORI
E28       1  AU=UEKI IR
E29       4  AU=UEKI IRIS
E30      12  AU=UEKI IRIS F
E31      89  AU=UEKI J
E32       4  AU=UEKI JUICHI
E33       8  AU=UEKI JUN
E34       3  AU=UEKI JUN-ICHI
E35       1  AU=UEKI JUNICHI
E36     468  AU=UEKI K

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?p

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E37       5  AU=UEKI KATSUJI
E38       9  AU=UEKI KAZUE
E39       2  AU=UEKI KAZUKO
E40       2  AU=UEKI KAZUYA
E41       1  AU=UEKI KEI
E42      39  AU=UEKI KEISUKE
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E43       22  AU=UEKI KEN
E44        1  AU=UEKI KENJI
E45        1  AU=UEKI KEU
E46        1  AU=UEKI KOHICHI
E47       31  AU=UEKI KOHJIRO
E48        1  AU=UEKI KOICHIRO

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E50        2  AU=UEKI KOJIRO
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Ref    Items  Index-term
E1         2  AU=UEKI KOJIRO
E2         3  AU=UEKI KOJIROH
E3         1  AU=UEKI KOUBUN
E4         2  AU=UEKI KOUICHIROU
E5         2  AU=UEKI KUNIKAZU
E6         1  AU=UEKI KUNIMASA
E7         3  AU=UEKI KYO
E8         2  AU=UEKI KYOKO
E9       418  AU=UEKI M
E10        6  AU=UEKI MAKOTO
E11       33  AU=UEKI MASAAKI
E12        1  AU=UEKI MASAKAI

          Enter P or PAGE for more
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Ref    Items  Index-term
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E15       11  AU=UEKI MASASHI
E16        6  AU=UEKI MASATO
E17        1  AU=UEKI MASAYA
E18        1  AU=UEKI MAYUMI
E19        2  AU=UEKI MICHIKO
E20       54  AU=UEKI MINORU
E21        1  AU=UEKI MISUZU
E22        3  AU=UEKI MITSUHIKO
E23       61  AU=UEKI N
E24        8  AU=UEKI NOBORU

          Enter P or PAGE for more
?p

Ref    Items  Index-term
E25        9  AU=UEKI NOBUHIDE
E26        1  AU=UEKI NORITAKA
E27        2  AU=UEKI NORIYUKI
E28       35  AU=UEKI O
E29        5  AU=UEKI OSAMU
E30       30  AU=UEKI R
E31        1  AU=UEKI REIKO
E32        3  AU=UEKI RIE
E33        2  AU=UEKI RYUSUKE
E34      990  AU=UEKI S
E35        1  AU=UEKI S S
E36        2  AU=UEKI S Y M

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?s e25
      S1         9  AU="UEKI NOBUHIDE"
?rd
...completed examining records
      S2         9  RD (unique items)
?t/3/all
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2/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12500720 BIOSIS NO.: 200000254222
Identification and characterization of human ZNF274 cDNA, which encodes a novel Kruppel-type zinc-finger protein having nucleolar targeting ability.
AUTHOR: Yano Kazuhiro; *Ueki Nobuhide*; Oda Tamaki; Seki Naohiko; Masuho Yasuhiko; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Genomics 65 (1):p75-80 April 1, 2000
MEDIUM: print.
ISSN: 0888-7543
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12369624 BIOSIS NO.: 200000123126
cDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase anchoring protein 95 (AKAP95) on chromosome 19p13.11-p13.12 region.
AUTHOR: Seki Naohiko; *Ueki Nobuhide*; Yano Kazuhiro; Saito Toshiyuki; Masuho Yasuhiko; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 45 (1):p31-37 2000
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12147353 BIOSIS NO.: 199900442202
Isolation, tissue expression, and chromosomal assignment of a human LIM protein gene, showing homology to rat Enigma homologue (ENH).
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Masuho Yasuhiko; Saito Toshiyuki; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 44 (4):p256-260 1999
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11994216 BIOSIS NO.: 199900274735
Isolation and characterization of a novel human gene (HFB30) which encodes a protein with a RING finger motif.
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Masuho Yasuhiko; Saito Toshiyuki; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-08**Japan
JOURNAL: Biochimica et Biophysica Acta 1445 (2):p232-236 May 14, 1999

ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11949082 BIOSIS NO.: 199900195191
Isolation and chromosomal assignment of human genes encoding cofactor of LIM homeodomain proteins, CLIM1 and CLIM2.
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Ohira Miki; Saito Toshiyuki; Masuho Yasuhiko; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 44 (2):p112-115 1999
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11793329 BIOSIS NO.: 199900039438
Selection system for genes encoding nuclear-targeted proteins.
AUTHOR: *Ueki Nobuhide*(a); Oda Tamaki; Kondo Maiko; Yano Kazuhiro; Noguchi Teruhisa; Muramatsu Masa-Aki
AUTHOR ADDRESS: (a)Biological Technol. Lab., Helix Res. Inst., Kisarazu-shi, Chiba 292-0812**Japan
JOURNAL: Nature Biotechnology 16 (13):p1338-1342 Dec., 1998
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11770540 BIOSIS NO.: 199900016649
NOLP: Identification of a novel human nucleolar protein and determination of sequence requirements for its nucleolar localization.
AUTHOR: *Ueki Nobuhide*(a); Kondo Maiko; Seki Naohiko; Yano Kazuhiro; Oda Tamaki; Masuho Yasuhiko; Murmatsu Masa-Aki
AUTHOR ADDRESS: (a)Pharmaceuticals Discovery Laboratory, Mitsubishi Chemical Corporation, Kamoshida-cho 1000, Aobu-**Japan
JOURNAL: Biochemical and Biophysical Research Communications 252 (1):p97-102 Nov. 9, 1998
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11266466 BIOSIS NO.: 199800047798
Recombinant thermostable cycloinulo-oligosaccharide fructanotransferase produced by Saccharomyces cerevisiae.
AUTHOR: Kanai Tamotsu; *Ueki Nobuhide*; Kawaguchi Tomoko; Teranishi Yutaka; Atomi Haruyuki; Tomorbaatar Chishignjamchuugjin; Ueda Mitsuyoshi; Tanaka Atsuo(a

AUTHOR ADDRESS: (a)Lab. Applied Biological Chem., Dep. Synthetic Chem. Biological Chem., Graduate Sch. Engineering,**Japan
JOURNAL: Applied and Environmental Microbiology 63 (12):p4956-4960 Dec., 1997
ISSN: 0099-2240
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

08996755 BIOSIS NO.: 199497005125
Distribution of bent DNA structures in the fission yeast centromere.
AUTHOR: *Ueki Nobuhide*; Momoi Hiroyuki; Yamada Hisami; Mizuno Takeshi(a
AUTHOR ADDRESS: (a)Lab. Mol. Microbiol., Sch. Agric., Nagoya Univ., Chikusa-ku, Nagoya 464**Japan
JOURNAL: Gene (Amsterdam) 132 (2):p247-250 1993
ISSN: 0378-1119
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
?s lexa(s)nuclear(w)localization(w)signal
2114 LEXA
438217 NUCLEAR
297004 LOCALIZATION
343956 SIGNAL
S3 3 LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
?rd
...completed examining records
S4 2 RD (unique items)
?t/9/all

4/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12639445 BIOSIS NO.: 200000392947
A genetic system for detection of protein nuclear import and export.
AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky Vitaly(a)
AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute for Cell and Development Biology, State University of New York, Stony Brook, NY, 11794-5215**USA
JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
MEDIUM: print
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: We have developed a simple genetic assay to detect active nuclear localization (NLS) and export signals (NES) on the basis of their function within yeast cells. The bacterial LexA protein was modified (mLexA) to abolish its intrinsic NLS and fused to the activation domain of the yeast Gal4p (Gal4AD) with or without the SV40 large T-antigen NLS. In the import assay, if a tested protein fused to mLexA-Gal4AD contains a functional NLS, it will enter the cell nucleus and activate the reporter gene expression. In the export assay, if a tested protein fused to mLexA-SV40 NLS-Gal4AD contains a functional NES, it will exit into the cytoplasm, decreasing the reporter gene expression. We tested this system with known NLS and NES and then used it to demonstrate a NES activity of the capsid protein of a plant geminivirus. This approach may help to identify, analyze, and select for proteins containing functional NLS and NES.

DESCRIPTORS:
MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular

Biophysics); Methods and Techniques
BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Geminivirus--Plant Viruses, Viruses, Microorganisms; Rhizobiaceae--Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms
ORGANISMS: Agrobacterium (Rhizobiaceae); Saccharomyces cerevisiae (Ascomycetes)--strain-L40; geminivirus (Geminivirus)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Fungi; Microorganisms; Nonvascular Plants; Plant Viruses; Plants; Viruses
CHEMICALS & BIOCHEMICALS: *LexA* protein--nuclear export, nuclear export signal, nuclear import, *nuclear* *localization* *signal*; nucleotoplasmic shuttle protein
METHODS & EQUIPMENT: PCR (polymerase chain reaction)--DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; Transformer site-directed mutagenesis kit--Clontech, laboratory equipment; nuclear export assay--Bioassays/Physiological Analysis, analytical method; nuclear import assay--Bioassays/Physiological Analysis, analytical method
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
03504 Genetics and Cytogenetics-Plant
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
33508 Virology-Plant Host Viruses
BIOSYSTEMATIC CODES:
02816 Geminivirus (1993-)
06509 Rhizobiaceae (1992-)
15100 Ascomycetes

4/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09503679 BIOSIS NO.: 199497512049
Sry is a transcriptional activator.
AUTHOR: Dubin Robert A(a); Ostrer Harry
AUTHOR ADDRESS: (a)Human Genetics Program, New York Univ. Med. Cent., 550 First Ave., MSB 136, New York, NY 10016**USA
JOURNAL: Molecular Endocrinology 8 (9):p1182-1192 1994
ISSN: 0888-8809
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The SRY gene functions as a genetic switch in gonadal ridge initiating testis determination. The mouse Sry and human SRY open reading frames (ORFs) share a conserved DNA-binding domain (the HMG-box) yet exhibit no additional homology outside this region. As judged by the accumulation of lacZ-SRY hybrid proteins in the nucleus, both the human and mouse SRY ORFs contain a *nuclear* *localization* *signal*. The mouse Sry HMG-box domain selectively binds the sequence NACAAT in vitro when challenged with a random pool of oligonucleotides and binds AACAAT with the highest affinity. When put under the control of a heterologous promotor, the mouse Sry gene activated transcription of a reporter gene containing multiple copies of the AACAAT binding site. Activation was likewise observed for a GAL4-responsive reporter gene, when the mouse Sry gene was linked to the DNA-binding domain of GAL4. Using this system, the activation function was mapped to a glutamine/histidine-rich domain. In addition, *LexA*-mouse Sry fusion genes activated a *LexA*-responsive reporter gene in yeast. In contrast, a GAL4-human SRY fusion gene did not cause transcriptional activation. These studies suggest that both the human and the mouse SRY ORFs encode nuclear, DNA-binding proteins and that the mouse Sry ORF can function as a transcriptional activator with separable DNA-binding and activator domains.

REGISTRY NUMBERS: 56-85-9: GLUTAMINE; 71-00-1: HISTIDINE
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Endocrine System (Chemical Coordination and Homeostasis); Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics);

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    Physiology; Reproductive System (Reproduction)
  BIOSYSTEMATIC NAMES: Fungi-Unspecified--Fungi, Plantae; Hominidae--
    Primates, Mammalia, Vertebrata, Chordata, Animalia; Muridae--Rodentia,
    Mammalia, Vertebrata, Chordata, Animalia
  ORGANISMS: fungi (Fungi - Unspecified); human (Hominidae); mouse
    (Muridae); yeast (Fungi - Unspecified)
  BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; fungi;
    humans; mammals; microorganisms; nonhuman mammals; nonhuman vertebrates
    ; nonvascular plants; plants; primates; rodents; vertebrates
  CHEMICALS & BIOCHEMICALS:   GLUTAMINE; HISTIDINE
MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data
  MISCELLANEOUS TERMS:   ACTIVATOR DOMAIN; DNA-BINDING DOMAIN; GAL4 -
    RESPONSIVE REPORTER GENE; GENETIC SWITCH; GLUTAMINE/HISTIDINE-RICH
    DOMAIN; GONADAL RIDGE; HMG-BOX; HOMOLOGY; LACZ-SRY HYBRID PROTEIN;
    LEXA-RESPONSIVE REPORTER GENE; NUCLEAR LOCALIZATION SIGNAL; NUCLEOTIDE
    SEQUENCE DATA; OPEN READING FRAME; TESTIS
CONCEPT CODES:
  02506   Cytology and Cytochemistry-Animal
  02508   Cytology and Cytochemistry-Human
  03504   Genetics and Cytogenetics-Plant
  03506   Genetics and Cytogenetics-Animal
  03508   Genetics and Cytogenetics-Human
  10010   Comparative Biochemistry, General
  10300   Replication, Transcription, Translation
  10506   Biophysics-Molecular Properties and Macromolecules
  12003   Physiology, General and Miscellaneous-Comparative (1970- )
  13012   Metabolism-Proteins, Peptides and Amino Acids
  13014   Metabolism-Nucleic Acids, Purines and Pyrimidines
  16504   Reproductive System-Physiology and Biochemistry
  17006   Endocrine System-Gonads and Placenta
  51522   Plant Physiology, Biochemistry and Biophysics-Chemical
            Constituents
  10062   Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
  10064   Biochemical Studies-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:
  15000   Fungi-Unspecified
  86215   Hominidae
  86375   Muridae
?s nuclear(w)localization(w)signal(2n)identif?
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          297004  LOCALIZATION
          343956  SIGNAL
         1249469  IDENTIF?
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...examined 50 records  (100)
...completed examining records
      S6      71  RD (unique items)
?t/9/1-5

 6/9/1     (Item 1 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

06724313   Genuine Article#: ARZ48   Number of References: 36
Title: *IDENTIFICATION* OF A *NUCLEAR*-*LOCALIZATION* *SIGNAL* OF A YEAST
   RIBOSOMAL-PROTEIN
Author(s): MORELAND RB; NAM HG; HEREFORD LM; FRIED HM
Corporate Source: UNIV N CAROLINA,DEPT BIOCHEM & NUTR/CHAPEL HILL//NC/27514
    ; UNIV N CAROLINA,DEPT CHEM/CHAPEL HILL//NC/27514; HARVARD UNIV,SCH
    MED,DANA FARBER CANC INST/BOSTON//MA/02115; HARVARD UNIV,SCH MED,DEPT
    MICROBIOL & GENET/BOSTON//MA/02115
Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED
    STATES OF AMERICA, 1985, V82, N19, P6561-6565
Language: ENGLISH   Document Type: ARTICLE
Geographic Location: USA
Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences
Journal Subject Category: MULTIDISCIPLINARY SCIENCES
Research Fronts: 85-2737 002   (GENE EXPRESSION AND OTHER CHARACTERIZATION
    STUDIES OF THE SYNTHESIS AND SECRETION OF CELL MEMBRANE PROTEINS AND
```

GLYCOPROTEINS)
85-4880 002 (UPTAKE AND ACCUMULATION OF VARIOUS PROTEINS BY THE CELL NUCLEUS)
85-1468 001 (IDENTIFICATION, EXPRESSION AND OTHER ANALYSES OF GENES FROM ESCHERICHIA-COLI K-12 MUTANTS)
85-4047 001 (CONFORMATIONAL AND STRUCTURAL STUDIES OF PEPTIDES AND PROTEINS)

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BONNER WM, 1975, V64, P421, J CELL BIOL
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CRAIG N, 1971, V229, P75, NATURE-NEW BIOL
DEROBERTIS EM, 1983, V32, P1021, CELL
DINGWALL C, 1982, V30, P449, CELL
FELDHERR CM, 1984, V99, P2216, J CELL BIOL
FRIED HM, 1985, V5, P99, MOL CELL BIOL
FRIED HM, 1981, V78, P238, P NATL ACAD SCI USA
GURDON JB, 1970, V176, P303, P ROY SOC LOND B BIO
HALL MN, 1984, V36, P1057, CELL
JONES EW, 1984, V18, P233, ANNU REV GENET
KALDERON D, 1984, V39, P499, CELL
KALDERON D, 1984, V311, P33, NATURE
KALTHOFF H, 1982, V21, P741, BIOCHEMISTRY-US
KAUFER NF, 1983, V11, P3123, NUCLEIC ACIDS RES
KESSLER SW, 1975, V115, P1617, J IMMUNOL
KILMARTIN JV, 1982, V93, P576, J CELL BIOL
LANFORD RE, 1984, V37, P801, CELL
MAGER WH, 1975, V402, P105, BIOCHIM BIOPHYS ACTA
MANDECKI W, 1981, V147, P694, J BACTERIOL
MEYUHAS O, 1980, V10, P113, GENE
MILLER JH, 1972, EXPT MOL GENETICS
OTAKA E, 1984, V195, P544, MOL GEN GENET
SABATINI DD, 1982, V92, P1, J CELL BIOL
SCHULTZ LD, 1983, V155, P8, J BACTERIOL
SILVER PA, 1984, V81, P5951, P NATL ACAD SCI USA
TEEM JL, 1984, V12, P8295, NUCLEIC ACIDS RES
TEEM JL, 1983, THESIS BRANDEIS U WA
WALTER P, 1984, V38, P5, CELL
WARNER JR, 1977, V11, P201, CELL
WARNER JR, 1985, V5, P1512, MOL CELL BIOL
WARNER JR, 1980, P889, RIBOSOMES STRUCTURE
WU RS, 1971, V51, P643, J CELL BIOL
WUNDERLICH F, 1972, V7, P220, J MEMBRANE BIOL

6/9/2 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13129833 BIOSIS NO.: 200100336982
HIV-1 infection requires a functional integrase NLS.
AUTHOR: Bouyac-Bertoia Michele; Dvorin Jeffrey D; Fouchier Ron A M; Jenkins Yonchu; Meyer Barbara E; Wu Lily I; Emerman Michael; Malim Michael H(a)
AUTHOR ADDRESS: (a)Department of Microbiology, University of Pennsylvania School of Medicine, Philadelphia, PA, 19104: malim@mail.med.upenn.edu** USA
JOURNAL: Molecular Cell 7 (5):p1025-1035 May, 2001
MEDIUM: print
ISSN: 1097-2765
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: HIV-1 is able to infect nondividing cells productively in part because the postentry viral nucleoprotein complexes are actively imported into the nucleus. In this manuscript, we *identify* a novel *nuclear* *localization* *signal* (NLS) in the viral integrase (IN) protein that is essential for virus replication in both dividing and non-dividing cells. The IN NLS stimulates the efficient nuclear accumulation of viral DNA as

well as virion-derived IN protein during the initial stages of infection but is dispensable for catalytic function. Because this NLS is required for infection irrespective of target cell proliferation, we suggest that interactions between uncoated viral nucleoprotein complexes and the host cell nuclear import machinery are critical for HIV-1 infection of all cells.

DESCRIPTORS:
MAJOR CONCEPTS: Enzymology (Biochemistry and Molecular Biophysics); Cell Biology; Infection
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms
ORGANISMS: HIV-1 {human immunodeficiency virus 1} (Retroviridae); human (Hominidae)--in vitro cell lines
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses
DISEASES: HIV-1 infection {human immunodeficiency virus 1 infection}--immune system disease, viral disease
CHEMICALS & BIOCHEMICALS: functional integrase NLS {functional integrase nuclear localization signal}; viral integrase protein
METHODS & EQUIPMENT: Western blotting--detection/labeling techniques, gene mapping; indirect immunofluorescence--detection/labeling techniques
ALTERNATE INDEXING: HIV Infections (MeSH)
CONCEPT CODES:
02502 Cytology and Cytochemistry-General
02508 Cytology and Cytochemistry-Human
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10802 Enzymes-General and Comparative Studies; Coenzymes
33506 Virology-Animal Host Viruses
34508 Immunology and Immunochemistry-Immunopathology, Tissue Immunology
36006 Medical and Clinical Microbiology-Virology
BIOSYSTEMATIC CODES:
02623 Retroviridae (1993-)
86215 Hominidae

6/9/3 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13127712 BIOSIS NO.: 200100334861
Nuclear import and DNA-binding activity of RFX1. Evidence for an autoinhibitory mechanism.
AUTHOR: Katan-Khaykovich Yael; Shaul Yosef(a)
AUTHOR ADDRESS: (a)Department of Molecular Genetics, The Weizmann Institute of Science, Rehovot, 76100: yosef.shaul@weizmann.ac.il**Israel
JOURNAL: European Journal of Biochemistry 268 (10):p3108-3116 May, 2001
MEDIUM: print
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: RFX1 binds and regulates the enhancers of a number of viruses and cellular genes. RFX1 belongs to the evolutionarily conserved RFX protein family that shares a DNA-binding domain and a conserved C-terminal region. In RFX1 this conserved region mediates dimerization, and is followed by a unique C-terminal tail, containing a highly acidic stretch. In HL-60 cells nuclear translocation of RFX1 is regulated by protein kinase C with unknown mechanisms. By confocal fluorescence microscopy, we have *identified* a nonclassical *nuclear* *localization* *signal* (NLS) at the extreme C-terminus. The adjacent 'acidic region', which showed no independent NLS activity, potentiated the function of the NLS. Subcellular fractionation showed that the tight association of RFX1 with the nucleus is mediated by its DNA-binding domain and enhanced by the dimerization domain. In contrast, the acidic region inhibited nuclear association, by down-regulating the DNA-binding activity of RFX1. These data suggest an autoinhibitory interaction, which may regulate the

function of RFX1 at the level of DNA binding. The C-terminal tail thus constitutes a composite localization domain, which on the one hand mediates nuclear import of RFX1, and on the other hand inhibits its association with the nucleus and binding to DNA. The participation of the acidic region in both activities suggests a mechanism by which the nuclear import and DNA-binding activity of RFX1 may be coordinately regulated by phosphorylation by kinases such as PKC.

REGISTRY NUMBERS: 141436-78-4: PROTEIN KINASE C
DESCRIPTORS:
MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: HL-60 cell line (Hominidae)
ORGANISMS: PARTS ETC: nucleus
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans; Mammals; Primates; Vertebrates
CHEMICALS & BIOCHEMICALS: DNA; RFX1; protein kinase C
METHODS & EQUIPMENT: confocal fluorescence microscopy--analytical method
MISCELLANEOUS TERMS: protein-DNA interaction
CONCEPT CODES:
02502 Cytology and Cytochemistry-General
02508 Cytology and Cytochemistry-Human
03502 Genetics and Cytogenetics-General
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10802 Enzymes-General and Comparative Studies; Coenzymes
BIOSYSTEMATIC CODES:
86215 Hominidae

6/9/4 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13116965 BIOSIS NO.: 200100324114
Nuclear localization of Schizosaccharomyces pombe Mcm2/Cdc19p requires MCM complex assembly.
AUTHOR: Pasion Sally G; Forsburg Susan L(a)
AUTHOR ADDRESS: (a)Molecular Biology and Virology Laboratory, Salk Institute for Biological Studies, La Jolla, CA, 92037: forsburg@salk.edu **USA
JOURNAL: Molecular Biology of the Cell 10 (12):p4043-4057 December, 1999
MEDIUM: print
ISSN: 1059-1524
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: The minichromosome maintenance (MCM) proteins MCM2-MCM7 are conserved eukaryotic replication factors that assemble in a heterohexameric complex. In fission yeast, these proteins are nuclear throughout the cell cycle. In studying the mechanism that regulates assembly of the MCM complex, we analyzed the cis and trans elements required for nuclear localization of a single subunit, Mcm2p. Mutation of any single mcm gene leads to redistribution of wild-type MCM subunits to the cytoplasm, and this redistribution depends on an active nuclear export system. We *identified* the *nuclear* *localization* *signal* sequences of Mcm2p and showed that these are required for nuclear targeting of other MCM subunits. In turn, Mcm2p must associate with other MCM proteins for its proper localization; nuclear localization of MCM proteins thus requires assembly of MCM proteins in a complex. We suggest that coupling complex assembly to nuclear targeting and retention ensures that only intact heterohexameric MCM complexes remain nuclear.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology
BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae
ORGANISMS: Schizosaccharomyces pombe (Ascomycetes)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Fungi; Microorganisms; Nonvascular Plants; Plants
CHEMICALS & BIOCHEMICALS: MCM2-Cdc19p--minichromosome maintenance proteins, nuclear localization; MCM2-MCM7--minichromosome maintenance proteins; minichromosome maintenance proteins {MCM}
MISCELLANEOUS TERMS: cell cycle
CONCEPT CODES:
10060 Biochemical Studies-General
02502 Cytology and Cytochemistry-General
02504 Cytology and Cytochemistry-Plant
51522 Plant Physiology, Biochemistry and Biophysics-Chemical Constituents
BIOSYSTEMATIC CODES:
15100 Ascomycetes

6/9/5 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13019003 BIOSIS NO.: 200100226152
Identification and characterization of a Drosophila nuclear proteasome regulator: A homolog of human 11 S REGgamma (PA28gamma).
AUTHOR: Masson Patrick; Andersson Oskar; Petersen Ulla-Maja; Young Patrick (a)
AUTHOR ADDRESS: (a)Department of Molecular Biology, Stockholm University, S-10691, Stockholm: patrick.young@molbio.su.se**Sweden
JOURNAL: Journal of Biological Chemistry 276 (2):p1383-1390 January 12, 2001
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: We report the cloning and characterization of a Drosophila proteasome 11 S REGgamma (PA28) homolog. The 28-kDa protein shows 47% identity to the human REGgamma and strongly enhances the trypsin-like activities of both Drosophila and mammalian 20 S proteasomes. Surprisingly, the Drosophila REG was found to inhibit the proteasome's chymotrypsin-like activity against the fluorogenic peptide succinyl-LLVY-7-amino-4-methylcoumarin. Immunocytological analysis reveals that the Drosophila REG is localized to the nucleus but is distributed throughout the cell when nuclear envelope breakdown occurs during mitosis. Through site-directed mutagenesis studies, we have *identified* a functional *nuclear* *localization* *signal* present in the homolog-specific insert region. The Drosophila PA28 NLS is similar to the oncogene c-Myc nuclear localization motif. Comparison between uninduced and innate immune induced Drosophila cells suggests that the REGgamma proteasome activator has a role independent of the invertebrate immune system. Our results support the idea that gamma class proteasome activators have an ancient conserved function within metazoans and were present prior to the emergence of the alpha and beta REG classes.

REGISTRY NUMBERS: 140879-24-9: PROTEASOME
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Methods and Techniques
BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia
ORGANISMS: Drosophila melanogaster (Diptera)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Arthropods; Insects; Invertebrates
CHEMICALS & BIOCHEMICALS: dREG-gamma--characterization, identification, nuclear proteasome regulator; proteasome--chymotrypsin-like activity, trypsin-like activity
METHODS & EQUIPMENT: DNA cloning--Recombinant DNA Technology, genetic method; site-directed mutagenesis--genetic method, mutagenesis, protein engineering
CONCEPT CODES:
10060 Biochemical Studies-General

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  10062   Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
  10064   Biochemical Studies-Proteins, Peptides and Amino Acids
  10802   Enzymes-General and Comparative Studies; Coenzymes
  64076   Invertebrata, Comparative and Experimental Morphology, Physiology
            and Pathology-Insecta-Physiology
BIOSYSTEMATIC CODES:
  75314   Diptera
?ds

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S2          9   RD (unique items)
S3          3   LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
S4          2   RD (unique items)
S5        124   NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6         71   RD (unique items)
?s s6 and lacz
             71  S6
          17783  LACZ
      S7      0  S6 AND LACZ
?s s6 and reporter
             71  S6
          44730  REPORTER
      S8      5  S6 AND REPORTER
?rd
...completed examining records
      S9      5  RD (unique items)
?t/9/all

 9/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12874064   BIOSIS NO.: 200100081213
A constitutive region is responsible for nuclear targeting of 4.1R:
 Modulation by alternative sequences results in differential intracellular
 localization.
AUTHOR: Luque Carlos M; Correas Isabel(a)
AUTHOR ADDRESS: (a)Centro de Biologia Molecular 'Severo Ochoa' (CSIC/UAM),
  Universidad Autonoma de Madrid, E-28049, Madrid: icorreas@cbm.uam.es**
  Spain
JOURNAL: Journal of Cell Science  113 (13):p2485-2495 July, 2000
MEDIUM: print
ISSN: 0021-9533
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Red blood cell protein 4.1, 4.1R, is an extreme variation on the
  theme of isoform multiplicity. The diverse 4.1R isoforms, mainly
  generated by alternative pre-mRNA splicing, are localized at different
  intracellular sites, including the nucleus. To characterize nonerythroid
  4.1 proteins lacking the most upstream translation initiation site,
  analyze their intracellular localization and define specific domains
  involved in differential intracellular targeting of 4.1R, we cloned 4.1
  cDNAs lacking that translation initiation site. Seven different 4.1R
  cDNAs were isolated. Four of these encoded 4.1R proteins localized
  predominantly to the nucleus and the other three localized to the
  cytoplasm. Three of the nuclear 4.1R isoforms did not contain the
  *nuclear* *localization* *signal* previously *identified* in the
  alternative exon 16. A comparative analysis of the exon composition of
  the naturally occurring 4.1R cDNAs cloned and of appropriate composite
  cDNA constructs, with the subcellular distribution of their respective
  products, demonstrated that a region encoded by constitutive exons, which
  is therefore common to all 4.1R isoforms and has been termed 'core
  region', had the capacity of localizing to the nucleus. This region was
  able to confer nuclear targeting to a cytosolic *reporter*. In protein
  4.1R isoforms, the nuclear targeting of the core region is modulated by
  the expression of alternative exons. Thus, exon 5-encoded sequences
  eclipsed nuclear entry of the core region, resulting in 4.1R isoforms
```

that predominantly distributed to the cytoplasm. Exon 5 was also able to confer cytoplasmic localization to a nuclear *reporter*. In protein 4.1R isoforms, when exons 5 and 16 were both expressed the nuclear targeting effect of exon 16 was dominant to the inhibitory effect observed by the expression of exon 5, yielding proteins that predominantly localized to the nucleus. Taken together, these results indicate that all 4.1R molecules contain a conserved region that is sufficient to target the protein to the nucleus, but that specific exon-encoded sequences modulate this capacity by acting in a hierarchical order.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Blood and Lymphatics (Transport and Circulation)
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: MOLT-4 cell line (Hominidae)--human T lymphoid cells
ORGANISMS: PARTS ETC: red blood cell--blood and lymphatics
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans; Mammals; Primates; Vertebrates
CHEMICALS & BIOCHEMICALS: 4.1R protein--alternative sequences, constitutive region, intracellular localization, nuclear targeting, red blood cell protein
CONCEPT CODES:
02508 Cytology and Cytochemistry-Human
02502 Cytology and Cytochemistry-General
02506 Cytology and Cytochemistry-Animal
10060 Biochemical Studies-General
15002 Blood, Blood-Forming Organs and Body Fluids-Blood and Lymph Studies
15004 Blood, Blood-Forming Organs and Body Fluids-Blood Cell Studies
BIOSYSTEMATIC CODES:
86215 Hominidae

9/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12779863 BIOSIS NO.: 200000533486
Gene activation by varicella-zoster virus IE4 protein requires its dimerization and involves both the Arginine-rich sequence, the central part, and the carboxyl-terminal cysteine-rich region.
AUTHOR: Baudoux Laurence; Defechereux Patricia; Rentier Bernard; Piette Jacques(a)
AUTHOR ADDRESS: (a)Laboratory of Fundamental Virology and Immunology, Institute of Pathology, University of Liege, B23, B-4000, Liege**Belgium
JOURNAL: Journal of Biological Chemistry 275 (42):p32822-32831 October 20, 2000
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Varicella-zoster virus (VZV) open reading frame 4-encoded protein (IE4) possesses transactivating properties for VZV genes as well as for those of heterologous viruses. Since most transcription factors act as dimers, IE4 dimerization was studied using the mammalian two-hybrid system. Introduction of mutations in the IE4 open reading frame demonstrated that both the central region and the carboxyl-terminal cysteine-rich domain were important for efficient dimerization. Within the carboxyl-terminal domain, substitution of amino acids encompassing residues 443-447 totally abolished dimerization. Gene activation by IE4 was studied by transient transfection with an IE4 expression plasmid and a *reporter* gene under the control of either the human immunodeficiency virus, type 1, long terminal repeat or the VZV thymidine kinase promoter. Regions of IE4 important for dimerization were also shown to be crucial for transactivation. In addition, the arginine-rich domains Rb and Rc of the amino-terminal region were also demonstrated to be important for transactivation, whereas the Ra domain as well as an acidic and

bZIP-containing regions were shown to be dispensable for gene transactivation. A nucleocytoplasmic shuttling of IE4 has also been characterized, involving a +nuclear+ +localization+ +signal+ +identified+ within the Rb domain and a nuclear export mechanism partially depending on Crm-1.

REGISTRY NUMBERS: 52-90-4Q: CYSTEINE; 3374-22-9Q: CYSTEINE; 9002-06-6: THYMIDINE KINASE
DESCRIPTORS:
MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Herpesviridae--Animal Viruses, Viruses, Microorganisms; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms
ORGANISMS: HeLa cell line (Hominidae); human immunodeficiency virus-1 (Retroviridae); varicella-zoster virus (Herpesviridae)--pathogen
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses
CHEMICALS & BIOCHEMICALS: amino acids; cysteine; plasmids; proteins; +reporter+ genes; thymidine kinase--promoter; transcription factors --functions; viral IE4 proteins--analysis, dimerization, functions, molecular regions, nucleocytoplasmic shuttling, structures; viral proteins--analysis, functions
MISCELLANEOUS TERMS: gene mutations; open reading frames; protein nuclear export mechanisms--analysis; viral gene activation mechanisms --analysis; viral genetics
CONCEPT CODES:
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
02508 Cytology and Cytochemistry-Human
03502 Genetics and Cytogenetics-General
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10802 Enzymes-General and Comparative Studies; Coenzymes
31500 Genetics of Bacteria and Viruses
33506 Virology-Animal Host Viruses
BIOSYSTEMATIC CODES:
02612 Herpesviridae (1993-)
02623 Retroviridae (1993-)
86215 Hominidae

9/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09975122 BIOSIS NO.: 199598430040
A polymorphic bipartite motif signals nuclear targeting of early auxin-inducible proteins related to PS-IAA4 from pea (Pisum sativum).
AUTHOR: Abel Steffen; Theologis Athanasios(a)
AUTHOR ADDRESS: (a)Plant Gene Expression Cent., 800 Buchanan Street, Albany, CA 94710++USA
JOURNAL: Plant Journal 8 (1):p87-96 1995
ISSN: 0960-7412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The plant hormone, indoleacetic acid (IAA), transcriptionally activates two early genes in pea, PS-IAA4/5 and PS-IAA6, that encode short-lived nuclear proteins. The identification of the nuclear localization signals (NLS) in PS-IAA4 and PS-IAA6 using progressive deletion analysis and site-directed mutagenesis is reported. A C-terminal SV40-type NLS is sufficient to direct the beta-glucuronidase +reporter+ to the nucleus of transiently transformed tobacco protoplasts, but is dispensible for nuclear localization of both proteins. The dominant and essential NLS in PS-IAA4 and PS-IAA6 overlap with a bipartite basic motif which is polymorphic and conserved in related proteins from other plant species, having the consensus sequence (KKNEK)KR-X-(24-71)-(RSXRK)/(RK/RK). Both basic elements of this motif in PS-IAA4, (KR-X-41-RSYRK), function interdependently as a bipartite NLS.

However, in PS-IAA6 (KKNEKKR-X-36-RKK) the upstream element of the corresponding motif contains additional basic residues which allow its autonomous function as an SV40-type monopartite NLS. The spacer-length polymorphism, X-(24-70), in respective bipartite NLS peptides of several PS-IAA4-like proteins from Arabidopsis thaliana does not affect nuclear targeting function. The structural and functional variation of the bipartite basic motif in PS-IAA4-like proteins supports the proposed integrated consensus of NLS.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Chemical Coordination and Homeostasis; Genetics; Physiology
BIOSYSTEMATIC NAMES: Leguminosae--Dicotyledones, Angiospermae, Spermatophyta, Plantae
ORGANISMS: Pisum sativum (Leguminosae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots; plants; spermatophytes; vascular plants
MISCELLANEOUS TERMS: FUNCTIONAL VARIATION; GENETIC TRANSFORMATION; *NUCLEAR* *LOCALIZATION* *SIGNAL* *IDENTIFICATION*; PHYTOHORMONE; PROGRESSIVE DELETION ANALYSIS; PS-IAA4-LIKE PROTEINS; SITE-DIRECTED MUTAGENESIS; STRUCTURAL VARIATION
CONCEPT CODES:
02504 Cytology and Cytochemistry-Plant
03504 Genetics and Cytogenetics-Plant
10060 Biochemical Studies-General
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
51514 Plant Physiology, Biochemistry and Biophysics-Growth Substances
51520 Plant Physiology, Biochemistry and Biophysics-Translocation, Accumulation
51522 Plant Physiology, Biochemistry and Biophysics-Chemical Constituents
BIOSYSTEMATIC CODES:
26260 Leguminosae

9/9/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09765420 BIOSIS NO.: 199598220338
Nucleo-cytoplasmic distribution of human hnRNP proteins: A search for the targeting domains in hnRNP A1.
AUTHOR: Weighardt Florian(a); Biamonti Giuseppe; Riva Silvano
AUTHOR ADDRESS: (a)Ist. Genetica Biochmica Evoluzionistica del, CNR, Univ. degli Studi di Pavia, Via Abbiategrasso **Italy
JOURNAL: Journal of Cell Science 108 (2):p545-555 1995
ISSN: 0021-9533
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: hnRNP A1 (34 kDa) is an RNA binding protein consisting of two tandemly arranged RNA binding domains C-terminally linked to a glycine-rich auxiliary domain (2 times RBDGly). A1 belongs to the set of polypeptides that bind nascent hnRNA in the nucleus to form the so called hnRNP complexes. These complexes seem to be involved both in pre-mRNA processing and in the nuclear export of mRNA. In fact A1. along with other hnRNP proteins, is exported from the nucleus probably bound to mRNA and is immediately re-imported. A1 nuclear re-import, which requires active transcription, is not mediated by a canonical *nuclear* *localization* *signal* (NLS). To *identify* the determinants of A1 subcellular localization we developed an expression vector for studying the localization. in transiently transfected cells, of the different structural motifs of A1 fused to a small *reporter* protein (chloramphenicol acetyltransferase, CAT; 26 kDa). We demonstrate that a 30 amino acid sequence in the glycine-rich domain (YNDFGNYNNQSSNFGPMKGGNFGGRSSGPY), which bears no resemblance to canonical NLS, is necessary and sufficient to target the protein to the nucleus. Our data suggest that this targeting sequence might act by mediating the interaction of A1 with a NLS-containing nuclear import complex. On the

other hand, the nuclear export of A1 requires at least one RNA binding domain in accord with the hypothesis that A1 exits from the nucleus bound to mRNA. We propose a mechanism for the nucleo-cytoplasmic shuttling of A1 that envisages a specific role for the different structural domains and can explain the dependence of nuclear import from active transcription.

REGISTRY NUMBERS: 9040-07-7: CHLORAMPHENICOL ACETYLTRANSFERASE
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics); Morphology; Physiology
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: Hominidae (Hominidae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans; mammals; primates; vertebrates
CHEMICALS & BIOCHEMICALS: CHLORAMPHENICOL ACETYLTRANSFERASE
MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data; nucleotide sequence
MISCELLANEOUS TERMS: CHLORAMPHENICOL ACETYLTRANSFERASE; HETEROGENEOUS NUCLEAR RNA; MESSENGER RNA; SHUTTLE MECHANISM; TRANSCRIPTION
CONCEPT CODES:
02508 Cytology and Cytochemistry-Human
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules
10806 Enzymes-Chemical and Physical
11108 Anatomy and Histology, General and Comparative-Microscopic and Ultramicroscopic Anatomy
12100 Movement (1971-)
13012 Metabolism-Proteins, Peptides and Amino Acids
13014 Metabolism-Nucleic Acids, Purines and Pyrimidines
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10054 Biochemical Methods-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:
86215 Hominidae

9/9/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08931054 BIOSIS NO.: 199396082555
The matrix protein of Newcastle disease virus localizes to the nucleus via a bipartite nuclear localization signal.
AUTHOR: Coleman Natalie A; Peeples Mark E(a)
AUTHOR ADDRESS: (a)Dep. Immunol./Microbiol., St. Luke's Med. Cent., 1653 West Congress Parkway, Chicago, IL 60612**USA
JOURNAL: Virology 195 (2):p596-607 1993
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Newcastle disease virus matrix (M) protein expressed from a cDNA clone is observed in the nucleus of transfected cells, displaying a localization pattern identical to that observed in virus-infected cells. To *identify* the *nuclear* *localization* *signal* (NLS) in the M protein, M gene mutants encoding deletion and amino acid substitution proteins were constructed and expressed transiently in COS-1 cells. Protein products were examined for intracellular localization using indirect immunofluorescence. Two basic amino acid clusters in the M protein were found to be required for nuclear localization since deletion of these basic clusters or substitution with random amino acids resulted in cytoplasmic localization. Substitution of pairs of basic amino acids with non-basic residues revealed that components from both basic regions are required for nuclear localization. This interdependence between two

basic clusters suggests that the NLS in the M protein belongs to the newly described class of "bipartite" NLSs. Unlike most NLSs, M protein sequences containing the critical basic amino acid clusters fused to two different cytoplasmic *reporter* proteins failed to transport these proteins to the nucleus.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Microbiology
BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Paramyxoviridae--Viruses; Retroviridae--Viruses
ORGANISMS: simian immunodeficiency virus (Retroviridae); Cercopithecidae (Cercopithecidae); Paramyxoviridae (Paramyxoviridae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman primates; nonhuman vertebrates; primates; vertebrates; viruses
MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data
MISCELLANEOUS TERMS: CELL TROPISM; ENV GENE; LYMPHOCYTE; MACROPHAGE
CONCEPT CODES:
02506 Cytology and Cytochemistry-Animal
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
33506 Virology-Animal Host Viruses
31500 Genetics of Bacteria and Viruses
BIOSYSTEMATIC CODES:
02617 Paramyxoviridae (1993-)
86205 Cercopithecidae
?ds

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S2          9   RD (unique items)
S3          3   LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
S4          2   RD (unique items)
S5        124   NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6         71   RD (unique items)
S7          0   S6 AND LACZ
S8          5   S6 AND REPORTER
S9          5   RD (unique items)
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          438217  NUCLEAR
          297004  LOCALIZATION
               4  SIGANL
          580197  ASSAY
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          297004  LOCALIZATION
          343956  SIGNAL
          580197  ASSAY
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?s s11 and lacz
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           17783  LACZ
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...completed examining records
     S13       2  RD (unique items)
?t/9/all

 13/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
```


12821664 BIOSIS NO.: 200100028813
Evaluation of a new tool for exploring podocyte biology: Mouse Nphs1 5' flanking region drives *lacZ* expression in podocytes.
AUTHOR: Moeller Marcus J; Kovari Iulia A; Holzman Lawrence B(a)
AUTHOR ADDRESS: (a)University of Michigan Medical School, 1560 Medical Science Research Building II, Ann Arbor, MI, 48109-0676:

lholzman@umich.edu**USA
JOURNAL: Journal of the American Society of Nephrology 11 (12):p2306-2314
December, 2000
MEDIUM: print
ISSN: 1046-6673
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Study of podocyte biology has been hampered by limitations in available experimental models that both recapitulate the in vivo phenotypes of this cell and can be readily and specifically manipulated at the molecular level. Transgenic manipulation of the podocyte represents one approach that might circumvent these limitations. The purpose of this study was to identify a promoter-enhancer that would direct the expression of transgenes in a podocyte-specific manner. The nephrin (Nphs1) promoter was considered a good candidate for this purpose, because nephrin was thought to be expressed exclusively in podocytes. Two independent BAC clones that contained the murine Nphs1 gene were identified. An 8.3-kb and a 5.4-kb fragment containing the 5' flanking promoter sequence were identified and characterized. Two constructs were generated by placing a bacterial *lacZ* reporter with a *nuclear* *localization* *signal* under the control of these two DNA fragments. Mice transgenic for both constructs were generated. Using a chemiluminescence *assay*, beta-galactosidase activity significantly above control was detected only in tissue homogenates of kidneys and brain of transgenic mice. In X-gal stained sections of transgenic adult kidneys, only podocyte nuclei expressed beta-galactosidase. In adult brain examined by tissue sectioning, beta-galactosidase activity was confined to a discrete area in the medulla. Identical patterns of beta-galactosidase expression were observed in multiple transgenic founders, suggesting that the expression pattern observed was independent of the site of transgene integration. The developmental expression of beta-galactosidase in transgenic embryos was also analyzed. Transgenes regulated by this promoter should be useful for studying the biology of gene products that regulate podocyte phenotype and function.

REGISTRY NUMBERS: 9031-11-2: BETA-GALACTOSIDASE; 65136-96-1: NEPHRIN
DESCRIPTORS:
MAJOR CONCEPTS: Urinary System (Chemical Coordination and Homeostasis)
BIOSYSTEMATIC NAMES: Muridae--Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: mouse (Muridae)
ORGANISMS: PARTS ETC: podocyte--excretory system; renal medulla--excretory system
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
CHEMICALS & BIOCHEMICALS: *LacZ*--expression; X-gal; beta-galactosidase; nephrin; nephrin promoter
GENE NAME: Nphs1 gene (Muridae)--flanking region
METHODS & EQUIPMENT: chemiluminescence assay--analytical method, detection/labeling techniques
CONCEPT CODES:
15504 Urinary System and External Secretions-Physiology and Biochemistry
02506 Cytology and Cytochemistry-Animal
03506 Genetics and Cytogenetics-Animal
10802 Enzymes-General and Comparative Studies; Coenzymes
BIOSYSTEMATIC CODES:
86375 Muridae

13/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09666463 BIOSIS NO.: 199598121381
Human foamy virus Bell transactivator contains a bipartite nuclear localization determinant which is sensitive to protein context and triple multimerization domains.

AUTHOR: Chang Jun; Lee Ki Jeong; Jang Kyung Lib; Lee Eun Kyeong; Baek Gwan Hyuk; Sung Young Chul(a)
AUTHOR ADDRESS: (a)Dep. Life Sci., Pohang Univ. Sci. Technol., Pohang 790-784**North Korea
JOURNAL: Journal of Virology 69 (2):p801-808 1995
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Bell protein of human foamy virus is a 300-amino-acid nuclear regulatory protein which transactivates the gene expression directed by the homologous long terminal repeat and the human immunodeficiency virus type I long terminal repeat. While previous reports suggested that the single basic domain of Bell from residues 211 to 222 and/or 209 to 226 is necessary and sufficient for efficient nuclear localization (L. K. Venkatesh, C. Yang, P. A. Theodorakis, and G. Chinnandurai, J. Virol. 67:161-169, 1993; F. He, J. D. Sun, E. D. Garrett, and B. R. Cullen, J. Virol. 67:1896-1904, 1993), our recent data showed that another basic domain, from amino acid residues 199 to 200, is also required for nuclear localization of Bell (C. W. Lee, C. Jun, K. J. Lee, and Y. C. Sung, J. Virol. 68:2708-2719, 1994). To clarify this discrepancy, we constructed various bell-*lacZ* chimeric constructs and several linker insertion mutants and determined their subcellular localization. When the region of Bell containing basic domains was placed at an internal site of the *lacZ* gene, the *nuclear* *localization* *signal* (NLS) of Bell consisted of two discontinuous basic regions separated by an intervening sequence. Moreover, insertion of specific amino acids between two basic regions disrupted the activity of the Bell NLS. On the other hand, Bell residues 199 and 200 were not required to direct the Bell-beta-galactosidase chimeric protein to the nucleus when the Bell NLS was appended to the amino terminus of beta-galactosidase. These results indicate that the function of the Bell NLS is sensitive to the protein context within which the sequence is present. In addition, we demonstrated that the Bell protein forms a multimeric complex in the nuclei of mammalian cells by using a sensitive in vivo protein-protein interaction *assay*. Mutational analyses revealed that the regions which mediate multimer formation map to three domains of Bell, i.e., residues 1 to 31, 42 to 82, and 82 to 111. Furthermore, our results show that the region of Bell from residues 202 to 226 prevents Bell from forming a multimeric complex.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Microbiology; Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Mammalia-Unspecified--Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Viruses
ORGANISMS: Mammalia (Mammalia - Unspecified); Retroviridae (Retroviridae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman vertebrates; vertebrates; viruses
MISCELLANEOUS TERMS: MAMMALIAN CELLS; TRANSCRIPTIONAL GENE REGULATION
CONCEPT CODES:
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules
31500 Genetics of Bacteria and Viruses
33506 Virology-Animal Host Viruses
02506 Cytology and Cytochemistry-Animal
BIOSYSTEMATIC CODES:
02623 Retroviridae (1993-)
85700 Mammalia-Unspecified
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S4	2	RD (unique items)
S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?

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S7           0   S6 AND LACZ
S8           5   S6 AND REPORTER
S9           5   RD (unique items)
S10          0   NUCLEAR(W)LOCALIZATION(W)SIGANL(2N)ASSAY
S11        200   NUCLEAR(W)LOCALIZATION(W)SIGNAL(S)ASSAY
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           44730  REPORTER
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          175110  FUSION
     S16      3  S15 AND FUSION
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     S17      3  RD (unique items)
?t/9/all

 17/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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11469998   BIOSIS NO.: 199800251330
Intrinsic transcriptional activation-inhibition domains of the polyomavirus
 enhancer binding protein 2/core binding factor alpha subunit revealed in
 the presence of the beta subunit.
AUTHOR: Kanno Tomohiko; Kanno Yuka; Chen Lin-Feng; Ogawa Eiko; Kim
  Woo-Young; Ito Yoshiaki(a)
AUTHOR ADDRESS: (a)Inst. Virus Res., Kyoto Univ., Shogo-ku, Kyoto 606++
  Japan
JOURNAL: Molecular and Cellular Biology  18 (5):p2444-2454 May, 1998
ISSN: 0270-7306
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A member of the polyomavirus enhancer binding protein 2/core
  binding factor (PEBP2/CBF) is composed of PEBP2alphaB1/AML1 (as the alpha
  subunit) and a beta subunit. It plays an essential role in definitive
  hematopoiesis and is frequently involved in the chromosomal abnormalities
  associated with leukemia. In the present study, we report functionally
  separable modular structures in PEBP2alphaB1 for DNA binding and for
  transcriptional activation. DNA binding through the Runt domain of
  PEBP2alphaB1 was hindered by the adjacent carboxy-terminal region, and
  this inhibition was relieved by interaction with the P subunit. Utilizing
  a *reporter* *assay* system in which both the alpha and beta subunits are
  required to achieve strong transactivation, we uncovered the presence of
  transcriptional activation and inhibitory domains in PEBP2alphaB1 that
  were only apparent in the presence of the beta subunit. The inhibitory
  domain keeps the full transactivation potential of full-length
  PEBP2alphaB1 below its maximum potential. *Fusion* of the transactivation
  domain of PEBP2alphaB1 to the yeast GAL4 DNA-binding domain conferred
  transactivation potential, but further addition of the inhibitory domain
  diminished the activity. These results suggest that the activity of the a
  subunit as a transcriptional activator is regulated intramolecularly as
  well as by the beta subunit. PEBP2alphaB1 and the beta subunit were
  targeted to the nuclear matrix via signals distinct from the *nuclear*
  *localization* *signal*. Moreover, the transactivation domain by itself
  was capable of associating with the nuclear matrix, which implies the
  existence of a relationship between transactivation and nuclear matrix
  attachment.

DESCRIPTORS:
  MAJOR CONCEPTS: Biochemistry and Molecular Biophysics
  CHEMICALS & BIOCHEMICALS:   polyomavirus enhancer binding protein 2/core
```

binding factor {PEBP2/CBF}--alpha subunit, beta subunit, transcription factor, transcriptional activation-inhibition domains
CONCEPT CODES:
10060 Biochemical Studies-General
03502 Genetics and Cytogenetics-General

17/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10609221 BIOSIS NO.: 199699230366
Analysis of the VPg-proteinase (NIa) encoded by tobacco etch potyvirus: Effects of mutations on subcellular transport, proteolytic processing, and genome amplification.
AUTHOR: Schaad Mary C; Haldeman-Cahil Ruth; Cronin Stephen; Carrington James C(a)
AUTHOR ADDRESS: (a)Dep. Biol., Texas A and M Univ., College Station, TX 77843**USA
JOURNAL: Journal of Virology 70 (10):p7039-7048 1996
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A mutational analysis was conducted to investigate the functions of the tobacco etch potyvirus VPg-proteinase (NIa) protein in vivo. The NIa N-terminal domain contains the VPg attachment site, whereas the C-terminal domain contains a picornavirus 3C-like proteinase. Cleavage at an internal site separating the two domains occurs in a subset of NIa molecules. The majority of NIa molecules in TEV-infected cells accumulate within the nucleus. By using a *reporter* *fusion* strategy, the NIa *nuclear* *localization* *signal* was mapped to a sequence within amino acid residues 40 to 49 in the VPg domain. Mutations resulting in debilitation of NIa nuclear translocation also debilitated genome amplification, suggesting that the NLS overlaps a region critical for RNA replication. The internal cleavage site was shown to be a poor substrate for NIa proteolysis because of a suboptimal sequence context around the scissile bond. Mutants that encoded NIa variants with accelerated internal proteolysis exhibited genome amplification defects, supporting the hypothesis that slow internal processing provides a regulatory function. Mutations affecting the VPg attachment site and proteinase activesite residues resulted in amplification-defective viruses. A transgenic complementation *assay* was used to test whether NIa supplied in trans could rescue amplification-defective viral genomes encoding altered NIa proteins. Neither cells expressing NIa alone nor cells expressing a series of NIa-containing polyproteins supported increased levels of amplification of the mutants. The lack of complementation of NIa-defective mutants is in contrast to previous results obtained with RNA polymerase (NIb)-defective mutants, which were relatively efficiently rescued in the transgenic complementation *assay*. It is suggested that, unlike NIb polymerase, NIa provides replicative functions that are cis preferential.
REGISTRY NUMBERS: 154907-71-8: VPG-PROTEINASE
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Microbiology; Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Potyvirus--Viruses; Solanaceae--Dicotyledones, Angiospermae, Spermatophyta, Plantae
ORGANISMS: tobacco etch potyvirus (Potyvirus); Nicotiana tabacum (Solanaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots; microorganisms; plants; spermatophytes; vascular plants; viruses
CHEMICALS & BIOCHEMICALS: VPG-PROTEINASE
MISCELLANEOUS TERMS: CULTIVAR-XANTHI; ENZYMOLOGY; GENOME AMPLIFICATION; MOLECULAR GENETICS; PROTEOLYTIC PROCESSING; RNA REPLICATION; SUBCELLULAR TRANSPORT; VPG-PROTEINASE
CONCEPT CODES:
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids

10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules
10806 Enzymes-Chemical and Physical
31500 Genetics of Bacteria and Viruses
33508 Virology-Plant Host Viruses
BIOSYSTEMATIC CODES:
02829 Potyvirus (1993-)
26775 Solanaceae

17/9/3 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11444021 21282977 PMID: 11279056
Starvation promotes nuclear accumulation of the hsp70 Ssa4p in yeast cells.
Chughtai ZS; Rassadi R; Matusiewicz N; Stochaj U
Department of Physiology, McGill University, Montreal, Province of Quebec H3G 1Y6, Canada.
Journal of biological chemistry (United States) Jun 8 2001, 276 (23) p20261-6, ISSN 0021-9258 Journal Code: HIV
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Nuclear import of proteins that are too large to passively enter the nucleus requires soluble factors, energy, and a *nuclear* *localization* *signal* (NLS). Nuclear protein transport can be regulated, and different forms of stress affect nucleocytoplasmic trafficking. As such, import of proteins containing a classical NLS is inhibited in starving yeast cells. In contrast, the hsp70 Ssa4p concentrates in nuclei upon starvation. Nuclear concentration of Ssa4p in starving cells is reversible, and transfer of stationary phase cells to fresh medium induces Ssa4p nuclear export. This export reaction represents an active process that is sensitive to oxidative stress. In starving cells, the N-terminal domain of Ssa4p mediates Ssa4p nuclear accumulation, and a short hydrophobic sequence, termed Star (for starvation), is sufficient to localize the *reporter* proteins green fluorescent protein or beta-galactosidase to nuclei. To determine whether nuclear accumulation of Star-beta-galactosidase depends on a specific nuclear carrier, we have analyzed its distribution in mutant yeast strains that carry a deletion of a single beta-importin gene. With this *assay* we have identified Nmd5p as a beta-importin required to concentrate Star-beta-galactosidase in nuclei when cells enter stationary phase.
Tags: Support, Non-U.S. Gov't
Descriptors: Cell Nucleus--metabolism--ME; *Heat-Shock Proteins 70 --metabolism--ME; *Recombinant *Fusion* Proteins--metabolism--ME; *Saccharomyces cerevisiae--metabolism--ME; *Starvation; Luminescent Proteins--metabolism--ME; Nuclear Localization Signal; Protein Transport
CAS Registry No.: 0 (Heat-Shock Proteins 70); 0 (Luminescent Proteins); 0 (Nuclear Localization Signal); 0 (Recombinant Fusion Proteins); 147336-22-9 (green fluorescent protein)
Record Date Created: 20010604
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S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6	71	RD (unique items)
S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
S9	5	RD (unique items)
S10	0	NUCLEAR(W)LOCALIZATION(W)SIGANL(2N)ASSAY
S11	200	NUCLEAR(W)LOCALIZATION(W)SIGNAL(S)ASSAY
S12	4	S11 AND LACZ
S13	2	RD (unique items)
S14	21	S11 AND REPORTER
S15	12	RD (unique items)

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S17          3   RD (unique items)
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          297004  LOCALIZATION
          343956  SIGNAL
           46337  SCREEN
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          297004  LOCALIZATION
          343956  SIGNAL
         1566330  DETEC?
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           44730  REPORTER
           17783  LACZ
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     S22       2  RD (unique items)
?t/9/all

 22/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12560938   BIOSIS NO.: 200000314440
Identification of a novel signal sequence that targets transmembrane
 proteins to the nuclear envelope inner membrane.
AUTHOR: Meyer Grit Angel; Radsak Klaus Dietrich
AUTHOR ADDRESS: (a)Institut fuer Virologie der Philipps-Universitaet,
  Robert-Koch-Strasse 17, 35037, Marburg**Germany
JOURNAL: Journal of Biological Chemistry  275 (6):p3857-3866 February 11,
2000
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Herpesvirus maturation requires translocation of glycoprotein B
  homologue from the endoplasmic reticulum to the inner nuclear membrane.
  Glycoprotein B of human cytomegalovirus was used in this context as a
  model protein. To identify a specific signal sequence within human
  cytomegalovirus glycoprotein B acting in a modular fashion, coding
  sequences were recombined with *reporter* proteins. Immunofluorescence
  and cell fractionation demonstrated that a short sequence element within
  the cytoplasmic tail of human cytomegalovirus glycoprotein B was
  sufficient to translocate the membrane protein CD8 to the inner nuclear
  membrane. This carboxyl-terminal sequence had no *detectable* *nuclear*
  *localization* *signal* activity for soluble beta-Galactosidase and could
  not be substituted by the nuclear localization signal of SV40 T antigen.
  For glycoprotein B of herpes simplex virus, a carboxyl-terminal element
  with comparable properties was found. Further experiments showed that the
  amino acid sequence DRLRHR of human cytomegalovirus glycoprotein B (amino
  acids 885-890) was sufficient for nuclear envelope translocation. Single
  residue mutations revealed that the arginine residues in positions 4 and
  6 of the DRLRHR sequence were essential for its function. These results
  support the view that transmembrane protein transport to the inner
  nuclear membrane is controlled by a mechanism different from that of
  soluble proteins.

DESCRIPTORS:
  MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular
    Biophysics); Membranes (Cell Biology); Methods and Techniques
```

BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Herpesviridae--Animal Viruses, Viruses, Microorganisms
ORGANISMS: COS7 cell line (Cercopithecidae)--African green monkey kidney cells, transfected; cytomegalovirus (Herpesviridae); herpes simplex virus (Herpesviridae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Primates ; Nonhuman Vertebrates; Primates; Vertebrates; Viruses
CHEMICALS & BIOCHEMICALS: glycoprotein B--amino acid sequence, analysis , inner nuclear membrane transport, novel signal sequence, transmembrane protein
METHODS & EQUIPMENT: cell fractionation--Histological/Cytological and Culture Techniques, cytological method; immunofluorescence--Spectrum Analysis Techniques, detection method
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
02502 Cytology and Cytochemistry-General
10050 Biochemical Methods-General
10060 Biochemical Studies-General
10502 Biophysics-General Biophysical Studies
33502 Virology-General; Methods
BIOSYSTEMATIC CODES:
02612 Herpesviridae (1993-)
86205 Cercopithecidae

22/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10385719 BIOSIS NO.: 199699006864
A nuclear GFP/beta-galactosidase fusion protein as a marker for morphogenesis in living Drosophila.
AUTHOR: Shiga Yasuhiro; Tanaka-Matakatsu Miho; Hayashi Shigeo(a)
AUTHOR ADDRESS: (a)Genet. Stock Res. Cent., Natl. Inst. Genet., Mishima, Shizuoka-ken 411**Japan
JOURNAL: Development Growth & Differentiation 38 (1):p99-106 1996
ISSN: 0012-1592
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A general, non-invasive method to trace morphogenesis in living Drosophila was developed. To label specific cells. green fluorescence protein (GFP) of jellyfish Aequorea victoria was expressed by the Gal4-UAS system. Green fluorescence from GFP fused to the *nuclear* *localization* *signal* was *detectable* in polytene larval tissue, but not in diploid tissue. Further fusion to bacterial beta-galactosidase produced GFPN-*lacZ*, which fluoresced brightly in several diploid larval and embryonic tissues. GFPN-*lacZ* was used to trace dynamic cell movement during the formation of the embryonic tracheal system. These results indicate that GFPN-*lacZ* can be used to mark specific cells to study cell movement and gene expression in living animals.

REGISTRY NUMBERS: 9031-11-2: BETA-GALACTOSIDASE
DESCRIPTORS:
MAJOR CONCEPTS: Development; Genetics; Molecular Genetics (Biochemistry and Molecular Biophysics); Physiology; Respiratory System (Respiration)
BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia
ORGANISMS: Drosophila melanogaster (Diptera)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; arthropods; insects; invertebrates
CHEMICALS & BIOCHEMICALS: BETA-GALACTOSIDASE
MISCELLANEOUS TERMS: EMBRYONIC DEVELOPMENT; GENE EXPRESSION; GREEN FLUORESCENCE PROTEIN; TRACHEAL SYSTEM
CONCEPT CODES:
03506 Genetics and Cytogenetics-Animal
10300 Replication, Transcription, Translation
16004 Respiratory System-Physiology and Biochemistry
25502 Developmental Biology-Embryology-General and Descriptive

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  64076   Invertebrata, Comparative and Experimental Morphology, Physiology
             and Pathology-Insecta-Physiology
  10064   Biochemical Studies-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:
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          297004  LOCALIZATION
          343956  SIGNAL
         2413566  DETERMIN?
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           17783  LACZ
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         1193985  TRANSPORT
         1249469  IDENTIF?
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?t/9/all

 28/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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11852619 BIOSIS NO.: 199900098728

Specific binding of the karyopherin Kap121p to a subunit of the nuclear pore complex containing Nup53p, Nup59p, and Nup170p.

AUTHOR: Marelli Marcello; Aitchison John D; Wozniak Richard W(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol., 5-14 Med. Sci. Build., Univ. Alberta, Edmonton, AB T6G 2H7**Canada

JOURNAL: Journal of Cell Biology 143 (7):p1813-1830 Dec. 28, 1998
ISSN: 0021-9525
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have identified a specific karyopherin docking complex within the yeast nuclear pore complex (NPC) that contains two novel, structurally related nucleoporins, Nup53p and Nup59p, and the NPC core protein Nup170p. This complex was affinity purified from cells expressing a functional Nup53p-protein A chimera. The localization of Nup53p, Nup59p, and Nup170p within the NPC by immunoelectron microscopy suggests that the Nup53p-containing complex is positioned on both the cytoplasmic and nucleoplasmic faces of the NPC core. In association with the isolated complex, we have also *identified* the *nuclear* *transport* factor Kap121p (Pse1p). Using in vitro binding assays, we showed that each of the nucleoporins interacts with one another. However, the association of Kap121p with the complex is mediated by its interaction with Nup53p. Moreover, Kap121p is the only beta-type karyopherin that binds Nup53p suggesting that Nup53p acts as a specific Kap121p docking site. Kap121p can be released from Nup53p by the GTP bound form of the small GTPase Ran. The physiological relevance of the interaction between Nup53p and Kap121p was further underscored by the observation that NUP53 mutations alter the subcellular distribution of Kap121p and the Kap121p-mediated import of a ribosomal L25 *reporter* protein. Interestingly, Nup53p is specifically phosphorylated during mitosis. This phenomenon is correlated with a transient decrease in perinuclear-associated Kap121p.

DESCRIPTORS:
  MAJOR CONCEPTS: Cell Biology
  BIOSYSTEMATIC NAMES: Fungi--Plantae
  ORGANISMS: yeast (Fungi)
  BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Fungi; Microorganisms;
    Nonvascular Plants; Plants
  CHEMICALS & BIOCHEMICALS: importin; karyopherin; nuclear pore complex;
    nuclear transport factor Kap121p; Nup170p; Nup53p; Nup59p
  MISCELLANEOUS TERMS: cell cycle; nuclear transport
CONCEPT CODES:
  02504 Cytology and Cytochemistry-Plant
  03504 Genetics and Cytogenetics-Plant
  10060 Biochemical Studies-General
  10502 Biophysics-General Biophysical Studies
BIOSYSTEMATIC CODES:
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           46337 SCREEN
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 30/1/1   (Item 1 from file: 5)
10710785
?t/9/all

 30/9/1   (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)

10710785   BIOSIS NO.: 199799331930
GLE2, a Saccharomyces cerevisiae homologue of the Schizosaccharomyces pombe
 export factor RAE1, is required for nuclear pore complex structure and
 function.
AUTHOR: Murphy Robert; Watkins Janis L; Wente Susan R(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol. Physiol., Box 8228, Washington Univ.
  Sch. Med., 660 South Euclid Ave., St. Louis**USA
JOURNAL: Molecular Biology of the Cell 7 (12):p1921-1937 1996
ISSN: 1059-1524
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To identify and characterize novel factors required for *nuclear*
  transport, a genetic *screen* was conducted in the yeast Saccharomyces
  cerevisiae. Mutations that were lethal in combination with a null allele
  of the gene encoding the nucleoporin Nup100p were isolated using a
  colony-sectoring assay. Three complementation groups of gle (for GLFG
  lethal) mutants were identified. In this report, the characterization of
  GLE2 is detailed. GLE2 encodes a 40.5-kDa polypeptide with striking
  similarity to that of Schizosaccharomyces pombe RAE1. In indirect
  immunofluorescence and nuclear pore complex fractionation experiments,
  Gle2p was associated with nuclear pore complexes. Mutated alleles of GLE2
  displayed blockage of polyadenylated RNA export; however, nuclear protein
  import was not apparently diminished. Immunofluorescence and thin-section
  electron microscopic analysis revealed that the nuclear pore complex and
  nuclear envelope structure was grossly perturbed in gle2 mutants. Because
  the clusters of herniated pore complexes appeared subsequent to the
  export block, the structural perturbations were likely indirect
  consequences of the export phenotype. Interestingly, a two-hybrid
  interaction was detected between Gle2p and Srp1p, the nuclear
  localization signal receptor, as well as Rip1p, a nuclear export
  signal-interacting protein. We propose that Gle2p has a novel role in
  mediating nuclear transport.

DESCRIPTORS:
  MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;

Membranes (Cell Biology)
BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae
ORGANISMS: Saccharomyces cerevisiae (Ascomycetes); Schizosaccharomyces pombe (Ascomycetes)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): fungi; microorganisms; nonvascular plants; plants
MISCELLANEOUS TERMS: Research Article; BIOCHEMISTRY AND BIOPHYSICS; CELL BIOLOGY; FUNCTION; GLE2; GLE2P; NUCLEAR ENVELOPE; NUCLEAR EXPORT SIGNAL-INTERACTING PROTEIN; NUCLEAR LOCALIZATION SIGNAL RECEPTOR; NUCLEAR PORE COMPLEX; NUCLEAR TRANSPORT; RAE1; RIP1P; SRP1P; STRUCTURE
CONCEPT CODES:
02504 Cytology and Cytochemistry-Plant
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
10508 Biophysics-Membrane Phenomena
51522 Plant Physiology, Biochemistry and Biophysics-Chemical Constituents
BIOSYSTEMATIC CODES:
15100 Ascomycetes

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 34/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12874064 BIOSIS NO.: 200100081213
A constitutive region is responsible for nuclear targeting of 4.1R: Modulation by alternative sequences results in differential intracellular localization.
AUTHOR: Luque Carlos M; Correas Isabel(a)
AUTHOR ADDRESS: (a)Centro de Biologia Molecular 'Severo Ochoa' (CSIC/UAM), Universidad Autonoma de Madrid, E-28049, Madrid: icorreas@cbm.uam.es** Spain
JOURNAL: Journal of Cell Science 113 (13):p2485-2495 July, 2000
MEDIUM: print
ISSN: 0021-9533
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Red blood cell protein 4.1, 4.1R, is an extreme variation on the theme of isoform multiplicity. The diverse 4.1R isoforms, mainly generated by alternative pre-mRNA splicing, are localized at different intracellular sites, including the nucleus. To characterize nonerythroid 4.1 proteins lacking the most upstream translation initiation site, analyze their intracellular localization and define specific domains involved in differential intracellular targeting of 4.1R, we cloned 4.1 cDNAs lacking that translation initiation site. Seven different 4.1R cDNAs were isolated. Four of these encoded 4.1R proteins localized predominantly to the nucleus and the other three localized to the cytoplasm. Three of the nuclear 4.1R isoforms did not contain the *nuclear* *localization* *signal* previously *identified* in the

alternative exon 16. A comparative analysis of the exon composition of the naturally occurring 4.1R cDNAs cloned and of appropriate composite cDNA constructs, with the subcellular distribution of their respective products, demonstrated that a region encoded by constitutive exons, which is therefore common to all 4.1R isoforms and has been termed 'core region', had the capacity of localizing to the nucleus. This region was able to confer nuclear targeting to a cytosolic *reporter*. In protein 4.1R isoforms, the nuclear targeting of the core region is modulated by the expression of alternative exons. Thus, exon 5-encoded sequences eclipsed nuclear entry of the core region, resulting in 4.1R isoforms that predominantly distributed to the cytoplasm. Exon 5 was also able to confer cytoplasmic localization to a nuclear *reporter*. In protein 4.1R isoforms, when exons 5 and 16 were both expressed the nuclear targeting effect of exon 16 was dominant to the inhibitory effect observed by the expression of exon 5, yielding proteins that predominantly localized to the nucleus. Taken together, these results indicate that all 4.1R molecules contain a conserved region that is sufficient to target the protein to the nucleus, but that specific exon-encoded sequences modulate this capacity by acting in a hierarchical order.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Blood and Lymphatics (Transport and Circulation)
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: MOLT-4 cell line (Hominidae)--human T lymphoid cells
ORGANISMS: PARTS ETC: red blood cell--blood and lymphatics
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans; Mammals; Primates; Vertebrates
CHEMICALS & BIOCHEMICALS: 4.1R protein--alternative sequences, constitutive region, intracellular localization, nuclear targeting, red blood cell protein
CONCEPT CODES:
02508 Cytology and Cytochemistry-Human
02502 Cytology and Cytochemistry-General
02506 Cytology and Cytochemistry-Animal
10060 Biochemical Studies-General
15002 Blood, Blood-Forming Organs and Body Fluids-Blood and Lymph Studies
15004 Blood, Blood-Forming Organs and Body Fluids-Blood Cell Studies
BIOSYSTEMATIC CODES:
86215 Hominidae

34/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12779863 BIOSIS NO.: 200000533486
Gene activation by varicella-zoster virus IE4 protein requires its dimerization and involves both the Arginine-rich sequence, the central part, and the carboxyl-terminal cysteine-rich region.
AUTHOR: Baudoux Laurence; Defechereux Patricia; Rentier Bernard; Piette Jacques(a)
AUTHOR ADDRESS: (a)Laboratory of Fundamental Virology and Immunology, Institute of Pathology, University of Liege, B23, B-4000, Liege**Belgium
JOURNAL: Journal of Biological Chemistry 275 (42):p32822-32831 October 20, 2000
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Varicella-zoster virus (VZV) open reading frame 4-encoded protein (IE4) possesses transactivating properties for VZV genes as well as for those of heterologous viruses. Since most transcription factors act as dimers, IE4 dimerization was studied using the mammalian two-hybrid system. Introduction of mutations in the IE4 open reading frame demonstrated that both the central region and the carboxyl-terminal

cysteine-rich domain were important for efficient dimerization. Within the carboxyl-terminal domain, substitution of amino acids encompassing residues 443-447 totally abolished dimerization. Gene activation by IE4 was studied by transient transfection with an IE4 expression plasmid and a *reporter* gene under the control of either the human immunodeficiency virus, type 1, long terminal repeat or the VZV thymidine kinase promoter. Regions of IE4 important for dimerization were also shown to be crucial for transactivation. In addition, the arginine-rich domains Rb and Rc of the amino-terminal region were also demonstrated to be important for transactivation, whereas the Ra domain as well as an acidic and bZIP-containing regions were shown to be dispensable for gene transactivation. A nucleocytoplasmic shuttling of IE4 has also been characterized, involving a *nuclear* *localization* *signal* *identified* within the Rb domain and a nuclear export mechanism partially depending on Crm-1.

REGISTRY NUMBERS: 52-90-4Q: CYSTEINE; 3374-22-9Q: CYSTEINE; 9002-06-6: THYMIDINE KINASE
DESCRIPTORS:
MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Herpesviridae--Animal Viruses, Viruses, Microorganisms; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms
ORGANISMS: HeLa cell line (Hominidae); human immunodeficiency virus-1 (Retroviridae); varicella-zoster virus (Herpesviridae)--pathogen
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses
CHEMICALS & BIOCHEMICALS: amino acids; cysteine; plasmids; proteins; *reporter* genes; thymidine kinase--promoter; transcription factors --functions; viral IE4 proteins--analysis, dimerization, functions, molecular regions, nucleocytoplasmic shuttling, structures; viral proteins--analysis, functions
MISCELLANEOUS TERMS: gene mutations; open reading frames; protein nuclear export mechanisms--analysis; viral gene activation mechanisms --analysis; viral genetics
CONCEPT CODES:
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
02508 Cytology and Cytochemistry-Human
03502 Genetics and Cytogenetics-General
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10802 Enzymes-General and Comparative Studies; Coenzymes
31500 Genetics of Bacteria and Viruses
33506 Virology-Animal Host Viruses
BIOSYSTEMATIC CODES:
02612 Herpesviridae (1993-)
02623 Retroviridae (1993-)
86215 Hominidae

34/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09975122 BIOSIS NO.: 199598430040
A polymorphic bipartite motif signals nuclear targeting of early auxin-inducible proteins related to PS-IAA4 from pea (Pisum sativum).
AUTHOR: Abel Steffen; Theologis Athanasios(a)
AUTHOR ADDRESS: (a)Plant Gene Expression Cent., 800 Buchanan Street, Albany, CA 94710**USA
JOURNAL: Plant Journal 8 (1):p87-96 1995
ISSN: 0960-7412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The plant hormone, indoleacetic acid (IAA), transcriptionally activates two early genes in pea, PS-IAA4/5 and PS-IAA6, that encode short-lived nuclear proteins. The identification of the nuclear

localization signals (NLS) in PS-IAA4 and PS-IAA6 using progressive deletion analysis and site-directed mutagenesis is reported. A C-terminal SV40-type NLS is sufficient to direct the beta-glucuronidase *reporter* to the nucleus of transiently transformed tobacco protoplasts, but is dispensible for nuclear localization of both proteins. The dominant and essential NLS in PS-IAA4 and PS-IAA6 overlap with a bipartite basic motif which is polymorphic and conserved in related proteins from other plant species, having the consensus sequence (KKNEK)KR-X-(24-71)-(RSXRK)/(RK/RK). Both basic elements of this motif in PS-IAA4, (KR-X-41-RSYRK), function interdependently as a bipartite NLS. However, in PS-IAA6 (KKNEKKR-X-36-RKK) the upstream element of the corresponding motif contains additional basic residues which allow its autonomous function as an SV40-type monopartite NLS. The spacer-length polymorphism, X-(24-70), in respective bipartite NLS peptides of several PS-IAA4-like proteins from Arabidopsis thaliana does not affect nuclear targeting function. The structural and functional variation of the bipartite basic motif in PS-IAA4-like proteins supports the proposed integrated consensus of NLS.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Chemical Coordination and Homeostasis; Genetics; Physiology
BIOSYSTEMATIC NAMES: Leguminosae--Dicotyledones, Angiospermae, Spermatophyta, Plantae
ORGANISMS: Pisum sativum (Leguminosae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots; plants; spermatophytes; vascular plants
MISCELLANEOUS TERMS: FUNCTIONAL VARIATION; GENETIC TRANSFORMATION; *NUCLEAR* *LOCALIZATION* *SIGNAL* *IDENTIFICATION*; PHYTOHORMONE; PROGRESSIVE DELETION ANALYSIS; PS-IAA4-LIKE PROTEINS; SITE-DIRECTED MUTAGENESIS; STRUCTURAL VARIATION
CONCEPT CODES:
02504 Cytology and Cytochemistry-Plant
03504 Genetics and Cytogenetics-Plant
10060 Biochemical Studies-General
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
51514 Plant Physiology, Biochemistry and Biophysics-Growth Substances
51520 Plant Physiology, Biochemistry and Biophysics-Translocation, Accumulation
51522 Plant Physiology, Biochemistry and Biophysics-Chemical Constituents
BIOSYSTEMATIC CODES:
26260 Leguminosae

34/9/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09765420 BIOSIS NO.: 199598220338
Nucleo-cytoplasmic distribution of human hnRNP proteins: A search for the targeting domains in hnRNP A1.
AUTHOR: Weighardt Florian(a); Biamonti Giuseppe; Riva Silvano
AUTHOR ADDRESS: (a)Ist. Genetica Biochmica Evoluzionistica del, CNR, Univ. degli Studi di Pavia, Via Abbiategrasso **Italy
JOURNAL: Journal of Cell Science 108 (2):p545-555 1995
ISSN: 0021-9533
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: hnRNP A1 (34 kDa) is an RNA binding protein consisting of two tandemly arranged RNA binding domains C-terminally linked to a glycine-rich auxiliary domain (2 times RBDGly). A1 belongs to the set of polypeptides that bind nascent hnRNA in the nucleus to form the so called hnRNP complexes. These complexes seem to be involved both in pre-mRNA processing and in the nuclear export of mRNA. In fact A1. along with other hnRNP proteins, is exported from the nucleus probably bound to mRNA and is immediately re-imported. A1 nuclear re-import, which requires active transcription, is not mediated by a canonical *nuclear*

localization *signal* (NLS). To *identify* the determinants of A1 subcellular localization we developed an expression vector for studying the localization. in transiently transfected cells, of the different structural motifs of A1 fused to a small *reporter* protein (chloramphenicol acetyltransferase, CAT; 26 kDa). We demonstrate that a 30 amino acid sequence in the glycine-rich domain (YNDFGNYNNQSSNFGPMKGGNFGGRSSGPY), which bears no resemblance to canonical NLS, is necessary and sufficient to target the protein to the nucleus. Our data suggest that this targeting sequence might act by mediating the interaction of A1 with a NLS-containing nuclear import complex. On the other hand, the nuclear export of A1 requires at least one RNA binding domain in accord with the hypothesis that A1 exits from the nucleus bound to mRNA. We propose a mechanism for the nucleo-cytoplasmic shuttling of A1 that envisages a specific role for the different structural domains and can explain the dependence of nuclear import from active transcription.

REGISTRY NUMBERS: 9040-07-7: CHLORAMPHENICOL ACETYLTRANSFERASE
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics); Morphology; Physiology
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: Hominidae (Hominidae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans; mammals; primates; vertebrates
CHEMICALS & BIOCHEMICALS: CHLORAMPHENICOL ACETYLTRANSFERASE
MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data; nucleotide sequence
MISCELLANEOUS TERMS: CHLORAMPHENICOL ACETYLTRANSFERASE; HETEROGENEOUS NUCLEAR RNA; MESSENGER RNA; SHUTTLE MECHANISM; TRANSCRIPTION
CONCEPT CODES:
02508 Cytology and Cytochemistry-Human
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules
10806 Enzymes-Chemical and Physical
11108 Anatomy and Histology, General and Comparative-Microscopic and Ultramicroscopic Anatomy
12100 Movement (1971-)
13012 Metabolism-Proteins, Peptides and Amino Acids
13014 Metabolism-Nucleic Acids, Purines and Pyrimidines
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10054 Biochemical Methods-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:
86215 Hominidae

34/9/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08931054 BIOSIS NO.: 199396082555
The matrix protein of Newcastle disease virus localizes to the nucleus via a bipartite nuclear localization signal.
AUTHOR: Coleman Natalie A; Peeples Mark E(a)
AUTHOR ADDRESS: (a)Dep. Immunol./Microbiol., St. Luke's Med. Cent., 1653 West Congress Parkway, Chicago, IL 60612**USA
JOURNAL: Virology 195 (2):p596-607 1993
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Newcastle disease virus matrix (M) protein expressed from a cDNA clone is observed in the nucleus of transfected cells, displaying a localization pattern identical to that observed in virus-infected cells.

To *identify* the *nuclear* *localization* *signal* (NLS) in the M protein, M gene mutants encoding deletion and amino acid substitution proteins were constructed and expressed transiently in COS-1 cells. Protein products were examined for intracellular localization using indirect immunofluorescence. Two basic amino acid clusters in the M protein were found to be required for nuclear localization since deletion of these basic clusters or substitution with random amino acids resulted in cytoplasmic localization. Substitution of pairs of basic amino acids with non-basic residues revealed that components from both basic regions are required for nuclear localization. This interdependence between two basic clusters suggests that the NLS in the M protein belongs to the newly described class of "bipartite" NLSs. Unlike most NLSs, M protein sequences containing the critical basic amino acid clusters fused to two different cytoplasmic *reporter* proteins failed to transport these proteins to the nucleus.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Microbiology
BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Paramyxoviridae--Viruses; Retroviridae--Viruses
ORGANISMS: simian immunodeficiency virus (Retroviridae); Cercopithecidae (Cercopithecidae); Paramyxoviridae (Paramyxoviridae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman primates; nonhuman vertebrates; primates; vertebrates; viruses
MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data
MISCELLANEOUS TERMS: CELL TROPISM; ENV GENE; LYMPHOCYTE; MACROPHAGE
CONCEPT CODES:
02506 Cytology and Cytochemistry-Animal
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
33506 Virology-Animal Host Viruses
31500 Genetics of Bacteria and Viruses
BIOSYSTEMATIC CODES:
02617 Paramyxoviridae (1993-)
86205 Cercopithecidae
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...completed examining records
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 39/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12639445   BIOSIS NO.: 200000392947
A genetic system for detection of protein nuclear import and export.
AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky
  Vitaly(a)
AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute
  for Cell and Development Biology, State University of New York, Stony
  Brook, NY, 11794-5215**USA
JOURNAL: Nature Biotechnology  18 (4):p433-437 April, 2000
MEDIUM: print
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: We have developed a simple genetic assay to detect active nuclear
  localization (NLS) and export signals (NES) on the basis of their
  function within yeast cells. The bacterial LexA protein was modified
  (mLexA) to abolish its intrinsic NLS and fused to the activation domain
  of the yeast Gal4p (Gal4AD) with or without the SV40 large T-antigen NLS.
  In the import assay, if a tested protein fused to mLexA-Gal4AD contains a
  functional NLS, it will enter the cell nucleus and activate the
  *reporter* gene expression. In the export assay, if a tested protein
  fused to mLexA-SV40 NLS-Gal4AD contains a functional NES, it will exit
  into the cytoplasm, decreasing the *reporter* gene expression. We tested
  this system with known NLS and NES and then used it to demonstrate a NES
  activity of the capsid protein of a plant geminivirus. This approach may
  help to identify, analyze, and select for proteins containing functional
  NLS and NES.

DESCRIPTORS:
  MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular
    Biophysics); Methods and Techniques
  BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Geminivirus--Plant
    Viruses, Viruses, Microorganisms; Rhizobiaceae--Gram-Negative Aerobic
    Rods and Cocci, Eubacteria, Bacteria, Microorganisms
  ORGANISMS: Agrobacterium (Rhizobiaceae);  Saccharomyces cerevisiae
    (Ascomycetes)--strain-L40;  geminivirus (Geminivirus)
  BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Fungi;
    Microorganisms; Nonvascular Plants; Plant Viruses; Plants; Viruses
```

CHEMICALS & BIOCHEMICALS: LexA protein--nuclear export, nuclear export signal, nuclear import, nuclear localization signal; nucleotoplasmic shuttle protein
METHODS & EQUIPMENT: PCR {polymerase chain reaction}--DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; Transformer site-directed mutagenesis kit--Clontech, laboratory equipment; nuclear export assay--Bioassays/Physiological Analysis, analytical method; *nuclear* *import* *assay*--Bioassays/Physiological Analysis, analytical method
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
03504 Genetics and Cytogenetics-Plant
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
33508 Virology-Plant Host Viruses
BIOSYSTEMATIC CODES:
02816 Geminivirus (1993-)
06509 Rhizobiaceae (1992-)
15100 Ascomycetes

39/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11383718 BIOSIS NO.: 199800165050
Nuclear import of the capsid protein of tomato yellow leaf curl virus (TYLCV) in plant and insect cells.
AUTHOR: Kunik Talya; Palanichelvam Karuppaiah; Czosnek Henryk; Citovsky Vitaly; Gafni Yedidya(a)
AUTHOR ADDRESS: (a)Dep. Genetics, Agric. Res. Organization, PO Box 6, Bet Dagan 50250**Israel
JOURNAL: Plant Journal 13 (3):p393-399 Feb., 1998
ISSN: 0960-7412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The tomato yellow leaf curl virus (TYLCV) found in Israel is a whitefly-transmitted monopartite geminivirus. Although geminiviruses have been found in the nuclei of phloem-associated cells, the mechanism of viral invasion is poorly understood. The possible role of the TYLCV capsid protein (CP), the only known component of the viral coat, in virus transport into the host cell nucleus was investigated by monitoring its specific nuclear accumulation in plant and insect cells. CP was fused to the beta-glucuronidase (GUS) *reporter* enzyme to *assay* *nuclear* *import* in petunia protoplasts, and micro-injection of purified fluorescently labeled CP was used to examine its nuclear uptake in Drosophila embryos. Both assays demonstrated that TYLCV CP is transported into plant-and insect-cell nuclei by an active process of nuclear import via a nuclear localization signal (NLS)-specific pathway. Using the GUS assay and deletion analysis, the TYLCV CP NLS sequence was identified in the amino-terminus of the protein.

REGISTRY NUMBERS: 9001-45-0: BETA-GLUCURONIDASE
DESCRIPTORS:
MAJOR CONCEPTS: Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia ; Geminivirus--Plant Viruses, Viruses, Microorganisms; Solanaceae--Dicotyledones, Angiospermae, Spermatophyta, Plantae
ORGANISMS: petunia (Solanaceae)--protoplasts; tomato yellow leaf curl virus {TYLCV} (Geminivirus); Drosophila (Diptera)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Angiosperms; Animals; Arthropods; Dicots; Insects; Invertebrates; Microorganisms; Plant Viruses; Plants; Spermatophytes; Vascular Plants; Viruses
CHEMICALS & BIOCHEMICALS: capsid protein
METHODS & EQUIPMENT: beta-glucuronidase assay method--genetic method
MISCELLANEOUS TERMS: nuclear import
CONCEPT CODES:

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  31500   Genetics of Bacteria and Viruses
  33508   Virology-Plant Host Viruses
  54510   Phytopathology-Diseases Caused by Viruses
BIOSYSTEMATIC CODES:
  02816   Geminivirus (1993- )
  26775   Solanaceae
  75314   Diptera
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       438217  NUCLEAR
       297004  LOCALIZATION
       343956  SIGNAL
         2766  NUCLEAR(W)LOCALIZATION(W)SIGNAL
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 42/3/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12639445 BIOSIS NO.: 200000392947
A genetic system for detection of protein nuclear import and export.
AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky Vitaly(a)
AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute for Cell and Development Biology, State University of New York, Stony Brook, NY, 11794-5215**USA
JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
MEDIUM: print
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

42/3/2 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10803379 99242601 PMID: 10225947
Phosphorylation regulates in vivo interaction and molecular targeting of serine/arginine-rich pre-mRNA splicing factors.
Yeakley JM; Tronchere H; Olesen J; Dyck JA; Wang HY; Fu XD
Division of Cellular and Molecular Medicine, Department and School of Medicine, University of California, San Diego, La Jolla, California 92093-0651, USA.
Journal of cell biology (UNITED STATES) May 3 1999, 145 (3) p447-55, ISSN 0021-9525 Journal Code: HMV
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
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S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
S9	5	RD (unique items)
S10	0	NUCLEAR(W)LOCALIZATION(W)SIGANL(2N)ASSAY
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S36	43	NUCLEAR(W)IMPORT(3N)ASSAY
S37	26	RD (unique items)

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S40        104   LEXA(S)(DELETE? OR MODIF?)
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S42          2   RD (unique items)
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 44/3/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12787454   BIOSIS NO.: 200000541077
Positive injury signals induce growth and prolong survival in Aplysia
 neurons.
AUTHOR: Zhang Xiao-Ping; Ambron Richard T(a)
AUTHOR ADDRESS: (a)Department of Anatomy and Cell Biology, Columbia
  University, W. 168th Street, 1204 Black Building, New York, NY, 10032**
  USA
JOURNAL: Journal of Neurobiology  45 (2):p84-94 November 5, 2000
MEDIUM: print
ISSN: 0022-3034
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English


 44/3/2     (Item 2 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12639445   BIOSIS NO.: 200000392947
A genetic system for *detection* of protein *nuclear* *import* and export.
AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky
  Vitaly(a)
AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute
  for Cell and Development Biology, State University of New York, Stony
  Brook, NY, 11794-5215**USA
JOURNAL: Nature Biotechnology  18 (4):p433-437 April, 2000
MEDIUM: print
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English


 44/3/3     (Item 3 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12362230   BIOSIS NO.: 200000115732
Diminished human immunodeficiency virus type 1 reverse transcription and
 nuclear transport in primary macrophages arrested in early G1 phase of
 the cell cycle.
AUTHOR: Kootstra Neeltje A; Zwart Bianca M; Schuitemaker Hanneke(a)
AUTHOR ADDRESS: (a)Dept. of Clinical Viral-Immunology, Central Laboratory
  of the Netherlands Red Cross Blood Transfusion Service, Plesmanlaan 125,
  1066 CX, Amsterdam**Netherlands
JOURNAL: Journal of Virology  74 (4):p1712-1717 Feb., 2000
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
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LANGUAGE: English
SUMMARY LANGUAGE: English
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49/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12073184 BIOSIS NO.: 199900368033
Enhancement of polylysine-mediated transferrinfection by nuclear localization sequences: Polylysine does not function as a nuclear localization sequence.
AUTHOR: Chan Chee Kai; Jans David A(a)
AUTHOR ADDRESS: (a)Nuclear Signalling Laboratory, Division for Biochemistry and Molecular Biology, John Curtin Scho**Australia
JOURNAL: Human Gene Therapy 10 (10):p1695-1702 July 1, 1999
ISSN: 1043-0342
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

49/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

09304821 BIOSIS NO.: 199497313191
A ligand-dependent bipartite nuclear targeting signal in the human androgen receptor: Requirement for the DNA-binding domain and modulation by NH-2-terminal and carboxyl-terminal sequences.
AUTHOR: Zhou Zhong-Xun; Sar Madhabananda; Simental Jorge A; Lane Malcolm V; Wilson Elizabeth M(a)
AUTHOR ADDRESS: (a)Lab. Reprod. Biol., CB 7500 ManNider Bldg., Univ. North Carolina, Chapel Hill, NC 27599**USA
JOURNAL: Journal of Biological Chemistry 269 (18):p13115-13123 1994
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
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49/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

09304821 BIOSIS NO.: 199497313191
A ligand-dependent bipartite nuclear targeting signal in the human androgen receptor: Requirement for the DNA-binding domain and modulation by NH-2-terminal and carboxyl-terminal sequences.

AUTHOR: Zhou Zhong-Xun; Sar Madhabananda; Simental Jorge A; Lane Malcolm V; Wilson Elizabeth M(a)
AUTHOR ADDRESS: (a)Lab. Reprod. Biol., CB 7500 ManNider Bldg., Univ. North Carolina, Chapel Hill, NC 27599**USA
JOURNAL: Journal of Biological Chemistry 269 (18):p13115-13123 1994
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The amino acid sequence requirements for androgen-dependent androgen receptor *nuclear* *import* were *determined* by immunostaining transiently expressed full-length wild-type and mutant human androgen receptors (AR) in monkey kidney COS cells and measuring transcriptional activity by cotransfection with a luciferase *reporter* vector in monkey kidney CV1 cells. Mutagenesis studies revealed a bipartite nuclear targeting sequence in the DNA binding and hinge regions at amino acids 617-633, consisting of two clusters of basic amino acids separated by 10 amino acids, RKCYEAGMTLGARKLKK. In a series of deletion mutants, AR NH-2-terminal fragments (residues 1-639 through 1-723) displayed constitutive nuclear import, and transcriptional activity was similar to that of the ligand-activated full-length wild type AR. In contrast, nuclear import and transcriptional activation were inhibited by sequence extensions into the steroid-binding domain (1-771). Constitutive nuclear import was regained in part by NH-2-terminal deletions of full-length AR. Expression of AR/pyruvate kinase chimeras defined a sequence required for predominant nuclear localization as residues 580-661, comprised of the second zinc finger region of the DNA-binding domain, the 17-amino-acid putative targeting sequence, and 28 residues of flanking carboxyl-terminal sequence. These studies suggest that the bipartite nuclear targeting sequence of AR includes flanking sequence and is modulated by interactions between the NH-2- and carboxyl-terminal regions.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Endocrine System (Chemical Coordination and Homeostasis); Genetics; Reproductive System (Reproduction)
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: Hominidae (Hominidae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans; mammals; primates; vertebrates
MISCELLANEOUS TERMS: AMINO-TERMINAL SEQUENCE; GENE REGULATION; MOLECULAR SEQUENCE
CONCEPT CODES:
03508 Genetics and Cytogenetics-Human
10067 Biochemical Studies-Sterols and Steroids
10506 Biophysics-Molecular Properties and Macromolecules
16504 Reproductive System-Physiology and Biochemistry
17006 Endocrine System-Gonads and Placenta
BIOSYSTEMATIC CODES:
86215 Hominidae
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              $44.55  27 Type(s) in Format  9
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   $113.91  Estimated total session cost   6.812 DialUnits


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